WE CLAIM:

1. A composition comprising a protein in crystalline form wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 4.

2. A composition according to claim 1 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 4.

3. A composition according to claim 1 wherein the protein consists consecutively of residues of SEQ. ID No. 4.

4. A composition according to claim 1 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

5. A composition according to claim 1 wherein the protein crystal has a crystal lattice in a $P2_1$ space group.

6. A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=79.9Å, b=56.9Å, c=95.2Å, α=90°, β=90.5°, and γ=90°.

7. A composition comprising a protein in crystalline form wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 5.

8. A composition according to claim 7 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 5.

9. A composition according to claim 7 wherein the protein consists consecutively of residues of SEQ. ID No. 5.

10. A composition according to claim 7 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

11. A composition according to claim 7 wherein the protein crystal has a crystal lattice in a $P2_12_12_1$ space group.

12. A composition according to claim 7 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=92.1Å, b= 97.6Å, c=138.9Å, and $\alpha=\beta=\gamma=90°$.

13. A composition comprising HDAC-2 in crystalline form wherein the crystal has a crystal lattice in a $P2_1$ space group.

14. A composition comprising HDAC-2 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=79.9Å, b=56.9Å, c=95.2Å, $\alpha=90°$, $\beta=90.5°$, and $\gamma=90°$.

15. A composition comprising HDAC-2 in crystalline form wherein the crystal has a crystal lattice in a $P2_12_12_1$ space group.

16. A composition comprising HDAC-2 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=92.1Å, b= 97.6Å, c=138.9Å, and $\alpha=\beta=\gamma=90°$.

17. A composition comprising a protein, wherein at least a portion of the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.

18. A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 4; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

19. A method according to claim 18 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 4.

20. A method according to claim 18 wherein at least a portion of the protein consists consecutively of residues of SEQ. ID No. 4.

21. A method according to claim 18 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

22. A method according to claim 18 wherein the protein crystal has a crystal lattice in a $P2_1$ space group.

23. A method according to claim 18 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=79.9Å, b=56.9Å, c=95.2Å, α=90°, β=90.5°, and γ=90°.

24. A method according to claim 18, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

25. A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 5; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

26. A method according to claim 25 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 5.

27. A method according to claim 25 wherein at least a portion of the protein consists consecutively of residues of SEQ. ID No. 5.

28. A method according to claim 25 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

29. A method according to claim 25 wherein the protein crystal has a crystal lattice in a $P2_12_12_1$ space group.

30. A method according to claim 25 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=92.1Å, b= 97.6Å, c=138.9Å, and α=β=γ=90°.

31. A method according to claim 25, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

32. A composition comprising an isolated protein consisting of SEQ. ID No. 4.

33. A composition according to claim 32 where the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.

34. A composition comprising an isolated protein consisting of SEQ. ID No. 4.

35. A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ. ID No. 4; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

36. A method according to claim 35 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 4.

37. A method according to claim 35 wherein the protein crystal has a crystal lattice in a $P2_1$ space group.

38. A method according to claim 35 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=79.9Å, b=56.9Å, c=95.2Å, α=90°, β=90.5°, and γ=90°.

39. A method according to claim 35, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

40. A method according to claim 35, the method further comprising measuring an activity of the protein when contacted with the one or more entities

41. A method according to claim 35, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present

42. A method according to claim 35, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.

43. A composition according to claim 42 where the protein is expressed from a nucleic acid molecule that comprises SEQ. ID No. 2.

44. A composition comprising an isolated protein consisting of SEQ. ID No. 5.

45. A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ. ID No. 5; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

46. A method according to claim 45 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 5.

47. A method according to claim 45 wherein at least a portion of the protein has at least 90% identity with SEQ. ID No. 5.

48. A method according to claim 45 wherein at least a portion of the protein has at least 95% identity with SEQ. ID No. 5.

49. A method according to claim 45, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

50. A method according to claim 45, the method further comprising measuring an activity of the protein when contacted with the one or more entities

51. A method according to claim 45, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present

52. A method according to claim 45, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.